



Full wwPDB NMR Structure Validation Report ⓘ

Apr 15, 2026 – 11:19 AM UTC

PDB ID : 1OVX / pdb_00001ovx
Title : NMR structure of the E. coli ClpX chaperone zinc binding domain dimer
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Deposited on : 2003-03-27

This is a Full wwPDB NMR Structure Validation Report for a publicly released PDB entry.

We welcome your comments at validation@mail.wwpdb.org

A user guide is available at

<https://www.wwpdb.org/validation/2017/NMRValidationReportHelp>

with specific help available everywhere you see the ⓘ symbol.

The types of validation reports are described at

<http://www.wwpdb.org/validation/2017/FAQs#types>.

The following versions of software and data (see [references ⓘ](#)) were used in the production of this report:

MolProbity : **FAILED**
Percentile statistics : 20250101.v01 (using entries in the PDB archive January 1st 2025)
wwPDB-RCI : v_1n_11_5_13_A (Berjanski et al., 2005)
PANAV : Wang et al. (2010)
wwPDB-ShiftChecker : v1.2
Ideal geometry (proteins) : Engh & Huber (2001)
Ideal geometry (DNA, RNA) : Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP) : 2.49

1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

SOLUTION NMR

The overall completeness of chemical shifts assignment was not calculated.

There are no overall percentile quality scores available for this entry.

The sequence quality summary graphics cannot be shown.

2 Ensemble composition and analysis ⓘ

This entry contains 1 models. Identification of well-defined residues and clustering analysis are not possible.

3 Entry composition

There are 2 unique types of molecules in this entry. The entry contains 1184 atoms, of which 588 are hydrogens and 0 are deuteriums.

- Molecule 1 is a protein called ATP-dependent Clp protease ATP-binding subunit clpX.

Mol	Chain	Residues	Atoms						Trace
1	A	38	Total	C	H	N	O	S	0
			591	187	294	50	55	5	
1	B	38	Total	C	H	N	O	S	0
			591	187	294	50	55	5	

There are 14 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	-6	GLY	-	expression tag	UNP P0A6H1
A	-5	HIS	-	expression tag	UNP P0A6H1
A	-4	HIS	-	expression tag	UNP P0A6H1
A	-3	HIS	-	expression tag	UNP P0A6H1
A	-2	HIS	-	expression tag	UNP P0A6H1
A	-1	HIS	-	expression tag	UNP P0A6H1
A	0	HIS	-	expression tag	UNP P0A6H1
B	-6	GLY	-	expression tag	UNP P0A6H1
B	-5	HIS	-	expression tag	UNP P0A6H1
B	-4	HIS	-	expression tag	UNP P0A6H1
B	-3	HIS	-	expression tag	UNP P0A6H1
B	-2	HIS	-	expression tag	UNP P0A6H1
B	-1	HIS	-	expression tag	UNP P0A6H1
B	0	HIS	-	expression tag	UNP P0A6H1

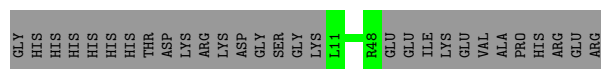
- Molecule 2 is ZINC ION (CCD ID: ZN) (formula: Zn).

Mol	Chain	Residues	Atoms	
2	A	1	Total	Zn
			1	1
2	B	1	Total	Zn
			1	1

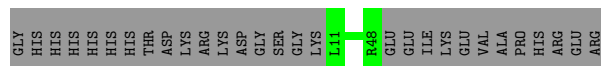
4 Residue-property plots

These plots are provided for all protein, RNA, DNA and oligosaccharide chains in the entry. The first graphic is the same as shown in the summary in section 1 of this report. The second graphic shows the sequence where residues are colour-coded according to the number of geometric quality criteria for which they contain at least one outlier: green = 0, yellow = 1, orange = 2 and red = 3 or more. Stretches of 2 or more consecutive residues without any outliers are shown as green connectors. Residues which are classified as ill-defined in the NMR ensemble, are shown in cyan with an underline colour-coded according to the previous scheme. Residues which were present in the experimental sample, but not modelled in the final structure are shown in grey.

- Molecule 1: ATP-dependent Clp protease ATP-binding subunit clpX



- Molecule 1: ATP-dependent Clp protease ATP-binding subunit clpX



5 Refinement protocol and experimental data overview ⓘ

The models were refined using the following method: *simulated annealing cartesian dynamics*.

Of the 500 calculated structures, 1 were deposited, based on the following criterion: *structures with acceptable covalent geometry*.

The following table shows the software used for structure solution, optimisation and refinement.

Software name	Classification	Version
X-PLOR	structure solution	NIH
X-PLOR	refinement	NIH

No chemical shift data was provided.

6 Model quality [i](#)

6.1 Standard geometry [i](#)

MolProbity failed to run properly - this section will have to be empty.

6.2 Too-close contacts [i](#)

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6.3 Torsion angles [i](#)

6.3.1 Protein backbone [i](#)

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6.3.2 Protein sidechains [i](#)

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6.3.3 RNA [i](#)

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6.4 Non-standard residues in protein, DNA, RNA chains [i](#)

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6.5 Carbohydrates [i](#)

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6.6 Ligand geometry [i](#)

MolProbity failed to run properly - this section will have to be empty.

6.7 Other polymers [i](#)

MolProbity failed to run properly - this section will have to be empty.

6.8 Polymer linkage issues

There are no chain breaks in this entry.

7 Chemical shift validation

No chemical shift data were provided